



PCT09

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RAW SEQUENCE LISTING

DATE: 04/11/2002

PATENT APPLICATION: US/09/913,898

TIME: 16:05:51

Input Set : A:\2001-11-12 1781-163P.txt

Output Set: N:\CRF3\04112002\I913898.raw

P.S

3 <110> APPLICANT: GONG, Zhiyuan
 4 LAM, Toong Jin
 5 JU, Bensheng
 6 XU, Yanfei
 7 HE, Jiangyan
 8 YAN, Tie

10 <120> TITLE OF INVENTION: CHIMERIC GENE CONSTRUCTS FOR GENERATION OF FLUORESCENT
 11 TRANSGENIC ORNAMENTAL FISH

12 <130> FILE REFERENCE: 1781-0163P

13 <140> CURRENT APPLICATION NUMBER: 09/913,898

C--> 14 <141> CURRENT FILING DATE: 2001-11-27

15 <150> PRIOR APPLICATION NUMBER: PCT/SG99/00079

16 <151> PRIOR FILING DATE: 1999-01-14

17 <160> NUMBER OF SEQ ID NOS: 24

18 <170> SOFTWARE: PatentIn Ver. 2.0

19 <210> SEQ ID NO: 1

20 <211> LENGTH: 2480

21 <212> TYPE: DNA

22 <213> ORGANISM: Danio rerio

23 <220> FEATURE:

24 <221> NAME/KEY: CDS

25 <222> LOCATION: (90)..(1586)

26 <220> FEATURE:

27 <221> NAME/KEY: primer_bind

28 <222> LOCATION: (66)..(85)

29 <223> OTHER INFORMATION: CK2

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31 <221> NAME/KEY: primer_bind

32 <222> LOCATION: (97)..(120)

33 <223> OTHER INFORMATION: CK1

34 <220> FEATURE:

35 <221> NAME/KEY: polyA_signal

36 <222> LOCATION: (2446)..(2451)

37 <400> SEQUENCE: 1

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 51 cttctcagca actcaaagac acaggcatc atg tca acc agg tct atc tct tac 113
 52 Met Ser Thr Arg Ser Ile Ser Tyr
 53 1 5

55 tcc agc ggt ggc tcc atc agg agg ggc tac acc agc cag tca gcc tat 161
 56 Ser Ser Gly Gly Ser Ile Arg Arg Gly Tyr Thr Ser Gln Ser Ala Tyr
 57 10 15 20

59 gca gta cct gcc ggc tct acc agg atg agc tca gtg acc agt gtc agg 209
 60 Ala Val Pro Ala Gly Ser Thr Arg Met Ser Ser Val Thr Ser Val Arg

ENTERED

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61	25		30		35		40	
63	aga tct ggt gtg ggt gcc agc cca ggc ttc ggt gcc ggt ggc agc tac	257						
64	Arg Ser Gly Val Gly Ala Ser Pro Gly Phe Gly Ala Gly Gly Ser Tyr							
65		45		50		55		
67	agc ttt agc agc agc agc atg ggt gga ggc tat gga agt ggt ctt ggt	305						
68	Ser Phe Ser Ser Ser Ser Met Gly Gly Tyr Gly Ser Gly Leu Gly							
69		60		65		70		
71	gga ggt ctc ggt ggg ggc atg ggc ttt cgt tgc ggg ctt cct atc aca	353						
72	Gly Gly Leu Gly Gly Gly Met Gly Phe Arg Cys Gly Leu Pro Ile Thr							
73		75		80		85		
75	gct gta act gtc aac cag aac ctg ttg gcc ccc tta aac ctg gaa atc	401						
76	Ala Val Thr Val Asn Gln Asn Leu Leu Ala Pro Leu Asn Leu Glu Ile							
77		90		95		100		
79	gac ccc aca att caa gct gtc cgc act tca gag aaa gag cag att aag	449						
80	Asp Pro Thr Ile Gln Ala Val Arg Thr Ser Glu Lys Glu Gln Ile Lys							
81	105		110		115		120	
83	acc ttc aac aac cgc ttc gct ttc ctc atc gac aaa gtg cgc ttc ctg	497						
84	Thr Phe Asn Asn Arg Phe Ala Phe Leu Ile Asp Lys Val Arg Phe Leu							
85		125		130		135		
87	gaa cag cag aac aag atg ctt gag acc aaa tgg agt ctt ctc caa gaa	545						
88	Glu Gln Gln Asn Lys Met Leu Glu Thr Lys Trp Ser Leu Leu Gln Glu							
89		140		145		150		
91	cag aca acc aca cgt tcc aac atc gat gcc atg ttt gag gca tac atc	593						
92	Gln Thr Thr Thr Arg Ser Asn Ile Asp Ala Met Phe Glu Ala Tyr Ile							
93		155		160		165		
95	tct aac ctg cgc aga cag ctc gat gga ctg gga aat gag aag atg aag	641						
96	Ser Asn Leu Arg Arg Gln Leu Asp Gly Leu Gly Asn Glu Lys Met Lys							
97		170		175		180		
99	ctg gag gga gag ctg aag aac atg cag ggc ctg gtt gag gac ttc aag	689						
100	Leu Glu Gly Glu Leu Lys Asn Met Gln Gly Leu Val Glu Asp Phe Lys							
101	185		190		195		200	
103	aac aag tac gag gat gag atc aac aag cgt gct tcc gta gag aat gag	737						
104	Asn Lys Tyr Glu Asp Glu Ile Asn Lys Arg Ala Ser Val Glu Asn Glu							
105		205		210		215		
107	ttt gtc ctg ctc aag aag gat gtt gat gca gcc tac atg aac aag gtt	785						
108	Phe Val Leu Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Asn Lys Val							
109		220		225		230		
111	gag ctt gaa gcc aag gtt gat gct ctt cag gat gag atc aac ttc ctc	833						
112	Glu Leu Glu Ala Lys Val Asp Ala Leu Gln Asp Glu Ile Asn Phe Leu							
113		235		240		245		
115	agg gca gtc tac gag gct gaa ctc cgg gag ctc cag tct cag atc aag	881						
116	Arg Ala Val Tyr Glu Ala Glu Leu Arg Glu Leu Gln Ser Gln Ile Lys							
117		250		255		260		
119	gac aca tct gtt gtt gta gaa atg gac aac agc aga aac ctg gat atg	929						
120	Asp Thr Ser Val Val Val Glu Met Asp Asn Ser Arg Asn Leu Asp Met							
121	265		270		275		280	
123	gac tcc atc gtg gct gaa gtt cgc gct cag tat gaa gac atc gcc aac	977						
124	Asp Ser Ile Val Ala Glu Val Arg Ala Gln Tyr Glu Asp Ile Ala Asn							
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127 cgc agc cgt gcc gag gca gag agc tgg tac aaa cag aag ttt gag gag 1025
128 Arg Ser Arg Ala Glu Ala Glu Ser Trp Tyr Lys Gln Lys Phe Glu Glu
129          300          305          310
131 atg cag agc acc gct ggt cag tat ggt gat gac ctc cgc tca aca aag 1073
132 Met Gln Ser Thr Ala Gly Gln Tyr Gly Asp Asp Leu Arg Ser Thr Lys
133          315          320          325
135 gct gag att gct gaa ctc aac cgc atg atc gcc cgc ctg cag aac gag 1121
136 Ala Glu Ile Ala Glu Leu Asn Arg Met Ile Ala Arg Leu Gln Asn Glu
137          330          335          340
139 atc gat gct gtc aag gca cag cgt gcc aac ttg gag gct cag att gct 1169
140 Ile Asp Ala Val Lys Ala Gln Arg Ala Asn Leu Glu Ala Gln Ile Ala
141 345          350          355          360
143 gag gct gaa gag cgt gga gag ctg gca gtg aag gat gcc aag ctc cgc 1217
144 Glu Ala Glu Glu Arg Gly Glu Leu Ala Val Lys Asp Ala Lys Leu Arg
145          365          370          375
147 atc agg gag ctg gag gaa gct ctt cag agg gcc aag caa gac atg gcc 1265
148 Ile Arg Glu Leu Glu Glu Ala Leu Gln Arg Ala Lys Gln Asp Met Ala
149          380          385          390
151 cgc cag gtc cgc gag tac cag gag ctc atg aac gtc aaa ttg gct ctg 1313
152 Arg Gln Val Arg Glu Tyr Gln Glu Leu Met Asn Val Lys Leu Ala Leu
153          395          400          405
155 gac att gag atc gcc acc tac agg aaa ctg ttg gaa gga gag gag agc 1361
156 Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu Ser
157          410          415          420
159 aga ctg tcc agc ggt gga gct caa gct acc att cat gtt cag cag acc 1409
160 Arg Leu Ser Ser Gly Gly Ala Gln Ala Thr Ile His Val Gln Gln Thr
161 425          430          435          440
163 tcc gga ggt gtt tca tct ggt tat ggt ggt agc ggc tct ggt ttc ggc 1457
164 Ser Gly Gly Val Ser Ser Gly Tyr Gly Gly Ser Gly Ser Gly Phe Gly
165          445          450          455
167 tac agc agt ggc ttc agc agt ggt ggg tca gga tac ggt agt gga tca 1505
168 Tyr Ser Ser Gly Phe Ser Ser Gly Gly Ser Gly Tyr Gly Ser Gly Ser
169          460          465          470
171 gga ttc ggt tct gga tca ggg tat ggt gga ggc tcc atc agc aaa acc 1553
172 Gly Phe Gly Ser Gly Ser Gly Tyr Gly Gly Gly Ser Ile Ser Lys Thr
173          475          480          485
175 agt gtc acc acc gtc agc agt aaa cgc tat taa ggagaagccc gcccaaacc 1606
176 Ser Val Thr Thr Val Ser Ser Lys Arg Tyr
177          490          495
179 ccagccgaca cagtttccaa ccttccttac ctgcaactag atcccttctg aaccttctta 1666
180 cgactcaaac catctatggt gctatatatt agccagacag ctgtcccctg ttaatgagga 1726
181 gatgtggacg atgattttta aagtacaaaa taagttagg attgttctgt gtgttgatgg 1786
182 tagttaccog tatcatgcat ctctgtctg gtggtgtcac tgccatttta aatcatcaac 1846
183 ccaactacac taaaacgata ccaggaagaa tcgtgctcca agccactgaa tagtcttatt 1906
184 tctgcaactga tatgtacagg gaaagtgaga cacatagaaa ccaactgtaac ctacgtagta 1966
185 ctatgggtttc actggatcag ggggtgtgcta tacaagttcc tgaatgtctt gtttgaatgt 2026
186 tttgtgctgt tacaagctcc ctgctgtagt tttgctgact aatctgactt ttgtcatttt 2086
187 gctatggctg tcagagttgg ttacctatt ttctataaaa tgtatatggc agtcagccaa 2146
188 taactgatga caattgcttg tgggctacta atgtccagtt acctcacatt caagggagat 2206

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189 ctgttacagc aaaaaacagg cacaatggga tttatgtgga ccatccctcc ttaaccttgt 2266
190 gtactttccg tgttggaagt ggtgactgta ctgccttaca cattcccctg tattcaactg 2326
191 gcttccagag catattttac atccccggtt ataaatggaa aatgcaagaa aactgaaaca 2386
192 atgttcaacc agattttatt ggtattgatt gacgagacac caacttgaaa tttgaataca 2446
193 ataaatctga gaccacaaaa aaaaaaaaaa aaaa 2480
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197 <211> LENGTH: 498
198 <212> TYPE: PRT
199 <213> ORGANISM: Danio rerio
201 <400> SEQUENCE: 2
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203 1 5 10 15
205 Gly Tyr Thr Ser Gln Ser Ala Tyr Ala Val Pro Ala Gly Ser Thr Arg
206 20 25 30
208 Met Ser Ser Val Thr Ser Val Arg Arg Ser Gly Val Gly Ala Ser Pro
210 35 40 45
212 Gly Phe Gly Ala Gly Gly Ser Tyr Ser Phe Ser Ser Ser Ser Met Gly
213 50 55 60
215 Gly Gly Tyr Gly Ser Gly Leu Gly Gly Gly Leu Gly Gly Gly Met Gly
216 65 70 75 80
218 Phe Arg Cys Gly Leu Pro Ile Thr Ala Val Thr Val Asn Gln Asn Leu
219 85 90 95
221 Leu Ala Pro Leu Asn Leu Glu Ile Asp Pro Thr Ile Gln Ala Val Arg
222 100 105 110
224 Thr Ser Glu Lys Glu Gln Ile Lys Thr Phe Asn Asn Arg Phe Ala Phe
225 115 120 125
227 Leu Ile Asp Lys Val Arg Phe Leu Glu Gln Gln Asn Lys Met Leu Glu
228 130 135 140
230 Thr Lys Trp Ser Leu Leu Gln Glu Gln Thr Thr Thr Arg Ser Asn Ile
231 145 150 155 160
233 Asp Ala Met Phe Glu Ala Tyr Ile Ser Asn Leu Arg Arg Gln Leu Asp
234 165 170 175
236 Gly Leu Gly Asn Glu Lys Met Lys Leu Glu Gly Glu Leu Lys Asn Met
237 180 185 190
239 Gln Gly Leu Val Glu Asp Phe Lys Asn Lys Tyr Glu Asp Glu Ile Asn
240 195 200 205
242 Lys Arg Ala Ser Val Glu Asn Glu Phe Val Leu Leu Lys Lys Asp Val
243 210 215 220
245 Asp Ala Ala Tyr Met Asn Lys Val Glu Leu Glu Ala Lys Val Asp Ala
246 225 230 235 240
248 Leu Gln Asp Glu Ile Asn Phe Leu Arg Ala Val Tyr Glu Ala Glu Leu
249 245 250 255
251 Arg Glu Leu Gln Ser Gln Ile Lys Asp Thr Ser Val Val Val Glu Met
252 260 265 270
254 Asp Asn Ser Arg Asn Leu Asp Met Asp Ser Ile Val Ala Glu Val Arg
255 275 280 285
257 Ala Gln Tyr Glu Asp Ile Ala Asn Arg Ser Arg Ala Glu Ala Glu Ser
258 290 295 300
260 Trp Tyr Lys Gln Lys Phe Glu Glu Met Gln Ser Thr Ala Gly Gln Tyr

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261 305          310          315          320
263 Gly Asp Asp Leu Arg Ser Thr Lys Ala Glu Ile Ala Glu Leu Asn Arg
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266 Met Ile Ala Arg Leu Gln Asn Glu Ile Asp Ala Val Lys Ala Gln Arg
267          340          345          350
269 Ala Asn Leu Glu Ala Gln Ile Ala Glu Ala Glu Glu Arg Gly Glu Leu
270          355          360          365
272 Ala Val Lys Asp Ala Lys Leu Arg Ile Arg Glu Leu Glu Glu Ala Leu
273          370          375          380
275 Gln Arg Ala Lys Gln Asp Met Ala Arg Gln Val Arg Glu Tyr Gln Glu
276 385          390          395          400
278 Leu Met Asn Val Lys Leu Ala Leu Asp Ile Glu Ile Ala Thr Tyr Arg
279          405          410          415
281 Lys Leu Leu Glu Gly Glu Glu Ser Arg Leu Ser Ser Gly Gly Ala Gln
282          420          425          430
284 Ala Thr Ile His Val Gln Gln Thr Ser Gly Gly Val Ser Ser Gly Tyr
285          435          440          445
287 Gly Gly Ser Gly Ser Gly Phe Gly Tyr Ser Ser Gly Phe Ser Ser Gly
288          450          455          460
290 Gly Ser Gly Tyr Gly Ser Gly Ser Gly Phe Gly Ser Gly Ser Gly Tyr
291 465          470          475          480
293 Gly Gly Gly Ser Ile Ser Lys Thr Ser Val Thr Thr Val Ser Ser Lys
294          485          490          495
296 Arg Tyr
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301 <212> TYPE: DNA
302 <213> ORGANISM: Danio rerio
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306 <222> LOCATION: (86)..(1231)
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310 <222> LOCATION: (6)..(26)
311 <223> OTHER INFORMATION: MCK2
313 <220> FEATURE:
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315 <222> LOCATION: (20)..(38)
316 <223> OTHER INFORMATION: MCK1
318 <220> FEATURE:
319 <221> NAME/KEY: polyA_signal
320 <222> LOCATION: (1534)..(1539)
322 <400> SEQUENCE: 3
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325 ttgtgcagtg ttagaaaccg caatc atg cct ttc gga aac acc cac aac aac 112
326          Met Pro Phe Gly Asn Thr His Asn Asn
327          1          5
329 ttc aag ctg aac tac tca gtt gat gag gag tat cca gac ctt agc aag 160
330 Phe Lys Leu Asn Tyr Ser Val Asp Glu Glu Tyr Pro Asp Leu Ser Lys

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.